



#11

SEQUENCE LISTING

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Peeters, Bernardus P.H.

<120> Mosaic Infectious Bursal Disease Virus Vaccines

<130> 2183-5238US

<140> US 10/046,671
<141> 2002-01-14

<150> PCT/NL00/00493
<151> 2000-07-13

<150> EP 99202316.8
<151> 1999-07-14

<160> 87

<170> PatentIn Ver. 2.1

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<211> 17

<212> DNA

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<223> Primer M13F-17

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<223> Primer AC4

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<223> Primer AC9

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24

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22

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21

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<223> Primer M13R

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<223> Primer

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<223> Primer ANC4"

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<210> 21

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<400> 21

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17

<210> 22

<211> 26

<212> DNA

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26

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<212> DNA

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<223> Primer HY3M

<400> 23

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21

<210> 24

<211> 17

<212> DNA

<213> Infectious bursal disease virus

<220>

<221> misc_feature

<223> Primer M13F

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<223> Primer HY4M

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<223> Primer ANC2

<400> 26
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<220>
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<223> Primer ANC3

<400> 28
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<220>
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<223> Primer ANC5

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cccatctgga gcatatcc 18

<210> 30
<211> 18
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<210> 31
<211> 30
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<222> (1)..(30)
<223> Anchor

<400> 31
cacgaattca ctatcgattc tggatccttc 30

<210> 32
<211> 20
<212> DNA
<213> Infectious bursal disease virus

<220>
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<222> (1)..(20)
<223> Anchor primer

<400> 32
gaaggatcca gaatcgatag 20

<210> 33
<211> 19
<212> DNA
<213> Infectious bursal disease virus

<220>
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<222> (1)..(19)
<223>Primer ANC0

<400> 33
ggggacccgc gaacggatc

19

<210> 34
<211> 16
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<220>
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16

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<222> (1)..(47)
<223> Primer T7AC0

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ggaattctaa tacgactcac tataggatac gatcggtctg accccgg

47

<210> 36
<211> 15
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<220>
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<222> (1)..(15)
<223> Primer BNC1

<400> 36

gggggcccc gcagg

15

<210> 37
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<400> 37

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45

<210> 38
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<220>
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of IBDV

<400> 38
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10

<210> 39
<211> 10
<212> RNA
<213> Infectious bursal disease virus

<220>
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<222> (1)..(10)
<223> 5'-Terminus of the A-segment coding strand
of IBDV

<400> 39
agauacgauc

10

<210> 40
<211> 10
<212> RNA
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<220>

<221> misc_RNA
 <222> (1)..(10)
 <223> 5'-Terminus of the A-segment coding strand
 of IBDV

 <400> 40
 ggauacgauc 10

 <210> 41
 <211> 10
 <212> RNA
 <213> Infectious bursal disease virus

 <220>
 <221> misc_RNA
 <222> (1)..(10)
 <223> Consensus sequence corresponding to the
 5'-terminus of the A-segment coding strand of
 IBDV

 <400> 41
 ggauacgauc 10

 <210> 42
 <211> 4
 <212> RNA
 <213> Infectious bursal disease virus

 <220>
 <221> misc_RNA
 <222> (1)..(4)
 <223> Complementary sequence of the 5'-terminus
 of the A-segment non-coding strand of IBDV

 <400> 42
 cggg 4

 <210> 43
 <211> 8
 <212> RNA
 <213> Infectious bursal disease virus

 <220>
 <221> misc_RNA
 <222> (1)..(8)
 <223> Complementary sequence of the 5'-terminus
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 <400> 43
 cggguccc 8

<210> 44
 <211> 9
 <212> RNA
 <213> Infectious bursal disease virus

 <220>
 <221> misc_RNA
 <222> (1)..(9)
 <223> Complementary sequence of the 5'-terminus
 of the A-segment non-coding strand of IBDV

<400> 44
 cgggucccu

9

<210> 45
 <211> 9
 <212> RNA
 <213> Infectious bursal disease virus

<220>
 <221> misc_RNA
 <222> (1)..(9)
 <223> Complementary sequence of the 5'-terminus
 of the A-segment non-coding strand of IBDV

<400> 45
 cgggucccc

9

<210> 46
 <211> 11
 <212> RNA
 <213> Infectious bursal disease virus

<220>
 <221> misc_RNA
 <222> (1)..(11)
 <223> Complementary sequence of the 5'-terminus
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<400> 46
 cggguccccc c

11

<210> 47
 <211> 12
 <212> RNA
 <213> Infectious bursal disease virus

<220>
 <221> misc_RNA
 <222> (1)..(12)
 <223> Complementary sequence of the 5'-terminus
 of the A-segment non-coding strand of IBDV

<400> 47
cggguccccc cu 12

<210> 48
<211> 12
<212> RNA
<213> Infectious bursal disease virus

<220>
<221> misc_RNA
<222> (1)..(12)
<223> Complementary sequence of the 5'-terminus
of the A-segment non-coding strand of IBDV

<400> 48
cggguccccc cc 12

<210> 49
<211> 9
<212> RNA
<213> Infectious bursal disease virus

<220>
<221> misc_RNA
<222> (1)..(9)
<223> Consensus complementary sequence of the
5'-terminus of the A-segment non-coding strand of
IBDV

<400> 49
cggguccccc 9

<210> 50
<211> 10
<212> RNA
<213> Infectious bursal disease virus

<220>
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<222> (1)..(10)
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of IBDV

<400> 50
ugauacgaug 10

<210> 51
<211> 10
<212> RNA
<213> Infectious bursal disease virus

<220>
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 <222> (1)..(10)
 <223> 5'-Terminus of the B-segment coding strand
 of IBDV

<400> 51
 ggauacgaug 10

<210> 52
 <211> 10
 <212> RNA

<213> Infectious bursal disease virus

<220>
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 <222> (1)..(10)
 <223> Consensus sequence of the 5'-terminus of
 the B-segment coding strand of IBDV

<400> 52
 ggauacgaug 10

<210> 53
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<220>
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 <222> (1)..(8)
 <223> Complementary sequence of the 5'-terminus
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<400> 53
 gggggcca 8

<210> 54
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<400> 54
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<220>
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<222> (1)..(8)
<223> Complementary sequence of the 5'-terminus
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<400> 55
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<210> 56
<211> 9
<212> RNA
<213> Infectious bursal disease virus

<220>
<221> misc_RNA
<222> (1)..(9)
<223> Complementary sequence of the 5'-terminus
of the B-segment non-coding strand of IBDV

<400> 56
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9

<210> 57
<211> 10
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<220>
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<222> (1)..(10)
<223> Complementary sequence of the 5'-terminus
of the B-segment non-coding strand of IBDV

<400> 57
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<210> 58
<211> 11
<212> RNA
<213> Infectious bursal disease virus

<220>
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<222> (1)..(11)

<223> Complementary sequence of the 5'-terminus
of the B-segment non-coding strand of IBDV

<400> 58
gggggcccc c 11

<210> 59
<211> 11
<212> RNA
<213> Infectious bursal disease virus

<220>
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<222> (1)..(11)
<223> Complementary sequence of the 5'-terminus
of the B-segment non-coding strand of IBDV

<400> 59
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<210> 60
<211> 10
<212> DNA
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<220>
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<222> (1)..(10)
<223> Consensus complementary sequence of the
5'-terminus of the B-segment non-coding strand of
IBDV

<400> 60
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<210> 61
<211> 119
<212> PRT
<213> Infectious bursal disease virus

<220>
<221> DOMAIN
<222> (1)..(119)
<223> Amino acid sequence of the hypervariable
region of VP2 of IBDV isolates D6948, rD6948, UK661
5123, 96-C6, 97-B4, 97-B5, 97-B6, Hungary, OKYM,
TKSM and HK46

<400> 61
Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Ala Gly Gly Val
1 5 10 15

Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser

20 25 30
 Ile Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Ile Leu
 35 40 45
 Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile Thr
 50 55 60
 Arg Ala Val Ala Ala Asp Asn Gly Leu Thr Ala Gly Thr Asp Asn Leu
 65 70 75 80
 Met Pro Phe Asn Ile Val Ile Pro Thr Ser Glu Ile Thr Gln Pro Ile
 85 90 95
 Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala
 100 105 110
 Gly Asp Gln Met Ser Trp Ser
 115

<210> 62
 <211> 119
 <212> PRT
 <213> Infectious bursal disease virus

<220>
 <221> DOMAIN
 <222> (1)..(119)
 <223> Amino acid sequence of the hypervariable
 region of VP2 of IBDV isolate 96-B4

<400> 62
 Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Pro Gly Gly Val
 1 5 10 15
 Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser
 20 25 30
 Val Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Val Leu
 35 40 45
 Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Thr Val Ile Thr
 50 55 60
 Arg Ala Val Ala Ala Asn Asn Gly Leu Thr Thr Gly Thr Asp Asn Leu
 65 70 75 80
 Leu Pro Phe Asn Ile Val Ile Pro Thr Asn Glu Ile Thr Gln Pro Ile
 85 90 95
 Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala
 100 105 110
 Gly Asp Gln Met Ser Trp Ser

115

<210> 63
<211> 119
<212> PRT
<213> Infectious bursal disease virus

<220>
<221> DOMAIN
<222> (1)..(119)
<223> Amino acid sequence of the hypervariable
region of VP2 of IBDV isolate 96-C4

<400> 63
Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Leu Gly Gly Val
1 5 10 15
Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser
20 25 30
Ile Gly Gly Glu Leu Val Phe Asn Thr Ser Val Gln Gly Leu Ala Leu
35 40 45
Asn Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Thr Val Ile Thr
50 55 60
Arg Ala Val Ala Ser Asp Asn Gly Leu Thr Thr Gly Ile Asp Asn Leu
65 70 75 80
Met Pro Phe Asn Ile Val Ile Pro Thr Asn Glu Ile Thr Gln Pro Ile
85 90 95
Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala
100 105 110
Gly Asp Gln Met Ser Trp Ser
115

<210> 64
<211> 119
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<213> Infectious bursal disease virus

<220>
<221> DOMAIN
<222> (1)..(119)
<223> Amino acid sequence of the hypervariable
region of VP2 of a IBDV isolate 96-C5

<400> 64
Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Pro Gly Gly Val
1 5 10 15

Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser
 20 25 30
 Val Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Val Leu
 35 40 45
 Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile Thr
 50 55 60
 Arg Ala Val Ala Ala Tyr Asn Gly Leu Thr Thr Gly Thr Asp Asn Leu
 65 70 75 80
 Leu Pro Phe Asn Ile Val Ile Pro Thr Asn Glu Ile Thr Gln Pro Ile
 85 90 95
 Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala
 100 105 110
 Gly Asp Gln Met Ser Trp Ser
 115

<210> 65
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 <213> Infectious bursal disease virus

<220>
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 <222> (1)..(119)
 <223> Amino acid sequence of the hypervariable
 region of VP2 of IBDV isolate 97-B3

<400> 65
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 Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser
 20 25 30
 Ile Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Ile Leu
 35 40 45
 Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile Thr
 50 55 60
 Arg Ala Val Ala Ala Asn Asn Gly Leu Thr Ala Gly Thr Asp Asn Leu
 65 70 75 80
 Met Pro Phe Asn Ile Val Ile Pro Thr Ser Glu Ile Thr Gln Pro Ile
 85 90 95
 Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala
 100 105 110

Gly Asp Gln Met Ser Trp Ser
115

<210> 66
<211> 119
<212> PRT
<213> Infectious bursal disease virus

<220>

<221> DOMAIN
<222> (1)..(119)
<223> Amino acid sequence of the hypervariable
region of VP2 of IBDV isolate Zoontjes

<400> 66
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1 5 10 15
Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser
20 25 30
Ile Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Ile Leu
35 40 45
Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile Thr
50 55 60
Arg Ala Val Ala Ala Asp Asn Gly Leu Thr Ala Gly Thr Asp Asn Leu
65 70 75 80
Met Pro Phe Asn Ile Val Ile Pro Thr Ser Glu Thr Thr Gln Pro Ile
85 90 95
Thr Ser Ile Lys Leu Val Ile Val Thr Ser Lys Ser Gly Gly Gln Ala
100 105 110
Gly Asp Gln Met Ser Trp Ser
115

<210> 67
<211> 119
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<213> Infectious bursal disease virus

<220>
<221> DOMAIN
<222> (1)..(119)
<223> Amino acid sequence of the hypervariable
region of VP2 of IBDV isolate OKYMT

<400> 67

Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Ala Gly Gly Val
1 5 10 15
Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser
20 25 30
Ile Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Thr Leu
35 40 45
Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile Thr
50 55 60
Arg Ala Val Ala Ala Asn Asn Gly Leu Thr Thr Gly Thr Asp Asn Leu
65 70 75 80
Met Pro Phe Asn Ile Val Ile Pro Thr Ser Glu Ile Thr Gln Pro Ile
85 90 95
Thr Ser Ile Lys Leu Glu Ile Val Thr Phe Lys Ser Gly Gly Gln Ala
100 105 110
Gly Asp Gln Met Ser Trp Ser
115

<210> 68
<211> 119
<212> PRT
<213> Infectious bursal disease virus

<220>
<221> DOMAIN
<222> (1)..(119)
<223> Amino acid sequence of the hypervariable
region of VP2 of IBDV isolate TKSMT

<400> 68
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1 5 10 15
Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser
20 25 30
Ile Gly Gly Glu Leu Val Phe His Thr Ser Val Gln Gly Leu Ile Leu
35 40 45
Asp Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Thr Thr
50 55 60
Arg Ala Val Ala Ala Asn Asn Gly Leu Thr Thr Gly Thr Asp Asn Leu
65 70 75 80
Met Pro Phe Asn Ile Val Ile Pro Thr Ser Glu Ile Thr Gln Pro Ile
85 90 95

Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala
100 105 110

Gly Asp Gln Met Ser Trp Ser
115

<210> 69
<211> 119
<212> PRT
<213> Infectious bursal disease virus

<220>
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<222> (1)..(119)
<223> Amino acid sequence of the hypervariable
region of VP2 of IBDV isolate HK46-NT

<400> 69
Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Ala Gly Gly Val
1 5 10 15

Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser
20 25 30

Ile Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Ile Leu
35 40 45

Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile Thr
50 55 60

Arg Ala Val Ala Ala Asn Asn Gly Leu Thr Thr Gly Thr Asp Asn Leu
65 70 75 80

Met Pro Phe Asn Ile Val Ile Pro Thr Ser Glu Ile Thr Gln Pro Ile
85 90 95

Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala
100 105 110

Gly Asp Gln Met Ser Trp Ser
115

<210> 70
<211> 3260
<212> DNA
<213> Infectious bursal disease virus

<220>
<221> misc_feature
<222> (1)..(3260)
<223> Consensus cDNA sequence of IBDV A-segment

<400> 70

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ccttctgatg	ccaacaaccg	gaccggcgtc	cattccggac	gacaccctrg	agaagcacac	240
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ggatccgttc gcgggtcccc                                     3260

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<210> 71
<211> 3260
<212> DNA
<213> Infectious bursal disease virus

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<220>
<221> misc_feature
<222> (1)..(3260)
<223> cDNA sequence CEF94-A of IBV A-segment

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<400> 71
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gatcgacgcg atgacaaacc tgcaagatca aaccaaacag attgttccgt tcatacggag 180
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ctactgcagg ctagtgaatc ggagtctcac agtgaggta agcacacttc ctggtggcgt 480
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<210> 72

<211> 3260

<212> DNA

<213> Infectious bursal disease virus

<220>

<221> misc_feature

<222> (1)..(3260)

<223> cDNA sequence D6948-A of IBV A-segment

<400> 72

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<210> 73

<211> 964

<212> DNA

<213> Infectious bursal disease virus

<220>

<221> misc_feature

<222> (1)..(964)

<223> cDNA sequence TY89-A of IBDV A-segment

<400> 73

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ccagaactcg aagacgctgt gcgtgcaatg gacgctgctg caaacgtcga cccattgttc 180
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caggccggaa gcaagtgcga gagggccaag tatggcacgg ctggctacgg agtggaggct 360
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aaggacctgc tcctgactgc gatggagatg aagcatcgca atcccaggcg ggctccacca 780
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cccc                                              964

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<210> 74
<211> 2827
<212> DNA
<213> Infectious bursal disease virus

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<220>
<221> misc_feature
<222> (1)..(2827)
<223> Consensus cDNA sequence of IBV B-segment

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caggagtact tcccwaarta ctaccaacaa caycgcccka gcaaggaraa gccaatgcg 480
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gccgagtggg cwagagytgc mgagttcggw gargcyttcg aaggcttcaa yatcaagctg 2160
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gtcaacagac cagtcaacac yggkgrctm aaggcagtc gcaaygcct caagaccggy 2280
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<210> 75

<211> 2827

<212> DNA

<213> Infectious bursal disease virus

<220>

<221> misc_feature

<222> (1)..(2827)

<223> cDNA sequence CEF94-B of IBV B-segment

<400> 75

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<210> 76

<211> 2827

<212> DNA

<213> Infectious bursal disease virus

<220>

<221> misc_feature

<222> (1)..(2827)

<223> cDNA sequence D6948-B of IBV B-segment

<400> 76

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<210> 77
<211> 1012
<212> PRT
<213> Infectious bursal disease virus

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<223> Consensus sequence of IBV polyprotein

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<223> The 'Xaa' at position 299 may be any amino acid

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<223> The 'Xaa' at position 451 may be any amino acid

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<223> The 'Xaa' at position 541 may be any amino acid

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<223> The 'Xaa' at position 680 may be any amino acid

<220>
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<223> The 'Xaa' at position 715 may be any amino acid

<400> 77

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 35 40 45
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 Gly Ser Ile Val Gly Ala His Tyr Thr Leu Gln Ser Asn Gly Asn Tyr
 65 70 75 80
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 Asn Tyr Cys Arg Leu Val Ser Arg Ser Leu Thr Val Arg Ser Ser Thr
 100 105 110
 Leu Pro Gly Gly Val Tyr Ala Leu Asn Gly Thr Ile Asn Ala Val Thr
 115 120 125
 Phe Gln Gly Ser Leu Ser Glu Leu Thr Asp Val Ser Tyr Asn Gly Leu
 130 135 140
 Met Ser Ala Thr Ala Asn Ile Asn Asp Lys Ile Gly Asn Val Leu Val
 145 150 155 160
 Gly Glu Gly Val Thr Val Leu Ser Leu Pro Thr Ser Tyr Asp Leu Gly
 165 170 175
 Tyr Val Arg Leu Gly Asp Pro Ile Pro Ala Ile Gly Leu Asp Pro Lys
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 Met Val Ala Thr Cys Asp Ser Ser Asp Arg Pro Arg Val Tyr Thr Ile
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 210 215 220
 Val Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu
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 Ser Xaa Gly Gly Glu Leu Val Phe Gln Thr Ser Val Xaa Gly Leu Xaa
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 260 265 270
 Thr Arg Ala Val Ala Ala Xaa Asn Gly Leu Thr Xaa Gly Thr Asp Asn
 275 280 285
 Leu Xaa Pro Phe Asn Xaa Val Ile Pro Thr Xaa Glu Ile Thr Gln Pro

290	295	300
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Ile His Gly Gly Asn Tyr Pro Gly Ala Leu Arg Pro Val Thr Leu Val 340 345 350		
Ala Tyr Glu Arg Val Ala Thr Gly Ser Val Val Thr Val Ala Gly Val 355 360 365		
Ser Asn Phe Glu Leu Ile Pro Asn Pro Glu Leu Ala Lys Asn Leu Val 370 375 380		
Thr Glu Tyr Gly Arg Phe Asp Pro Gly Ala Met Asn Tyr Thr Lys Leu 385 390 395 400		
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Arg Glu Tyr Thr Asp Phe Arg Glu Tyr Phe Met Glu Val Ala Asp Leu 420 425 430		
Asn Ser Pro Leu Lys Ile Ala Gly Ala Phe Gly Phe Lys Asp Ile Ile 435 440 445		
Arg Ala Xaa Arg Arg Ile Ala Val Pro Val Val Ser Thr Leu Phe Pro 450 455 460		
Pro Ala Ala Pro Leu Ala His Ala Ile Gly Glu Gly Val Asp Tyr Leu 465 470 475 480		
Leu Gly Asp Glu Ala Gln Ala Ala Ser Gly Thr Ala Arg Ala Ala Ser 485 490 495		
Gly Lys Ala Arg Ala Ala Ser Gly Arg Ile Arg Gln Leu Thr Leu Ala 500 505 510		
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Val Val Ile Thr Thr Val Glu Asp Ala Met Thr Pro Lys Ala Leu Asn 565 570 575		
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Met	Ala	Asn	Phe	Ala	Leu	Ser	Asp	Pro	Asn	Ala	His	Arg	Met	Arg	Asn	805	810	815
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Tyr	Gly	Thr	Ala	Gly	Tyr	Gly	Val	Glu	Ala	Arg	Gly	Pro	Thr	Pro	Glu	835	840	845
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85										90					95															
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Arg	Glu	Tyr	Thr	Asp	Phe	Arg	Glu	Tyr	Phe	Met	Glu	Val	Ala	Asp	Leu	420	425	430	
Asn	Ser	Pro	Leu	Lys	Ile	Ala	Gly	Ala	Phe	Gly	Phe	Lys	Asp	Ile	Ile	435	440	445	
Arg	Ala	Ile	Arg	Arg	Ile	Ala	Val	Pro	Val	Val	Ser	Thr	Leu	Phe	Pro	450	455	460	
Pro	Ala	Ala	Pro	Leu	Ala	His	Ala	Ile	Gly	Glu	Gly	Val	Asp	Tyr	Leu	465	470	475	480
Leu	Gly	Asp	Glu	Ala	Gln	Ala	Ala	Ser	Gly	Thr	Ala	Arg	Ala	Ala	Ser	485	490	495	
Gly	Lys	Ala	Arg	Ala	Ala	Ser	Gly	Arg	Ile	Arg	Gln	Leu	Thr	Leu	Ala	500	505	510	
Ala	Asp	Lys	Gly	Tyr	Glu	Val	Val	Ala	Asn	Leu	Phe	Gln	Val	Pro	Gln	515	520	525	
Asn	Pro	Val	Val	Asp	Gly	Ile	Leu	Ala	Ser	Pro	Gly	Val	Leu	Arg	Gly	530	535	540	
Ala	His	Asn	Leu	Asp	Cys	Val	Leu	Arg	Glu	Gly	Ala	Thr	Leu	Phe	Pro	545	550	555	560
Val	Val	Ile	Thr	Thr	Val	Glu	Asp	Ala	Met	Thr	Pro	Lys	Ala	Leu	Asn	565	570	575	
Ser	Lys	Met	Phe	Ala	Val	Ile	Glu	Gly	Val	Arg	Glu	Asp	Leu	Gln	Pro	580	585	590	
Pro	Ser	Gln	Arg	Gly	Ser	Phe	Ile	Arg	Thr	Leu	Ser	Gly	His	Arg	Val	595	600	605	
Tyr	Gly	Tyr	Ala	Pro	Asp	Gly	Val	Leu	Pro	Leu	Glu	Thr	Gly	Arg	Asp	610	615	620	
Tyr	Thr	Val	Val	Pro	Ile	Asp	Asp	Val	Trp	Asp	Asp	Ser	Ile	Met	Leu	625	630	635	640
Ser	Lys	Asp	Pro	Ile	Pro	Pro	Ile	Val	Gly	Asn	Ser	Gly	Asn	Leu	Ala	645	650	655	
Ile	Ala	Tyr	Met	Asp	Val	Phe	Arg	Pro	Lys	Val	Pro	Ile	His	Val	Ala	660	665	670	

Met Thr Gly Ala Leu Asn Ala Cys Gly Glu Ile Glu Lys Val Ser Phe
 675 680 685
 Arg Ser Thr Lys Leu Ala Thr Ala His Arg Leu Gly Leu Lys Leu Ala
 690 695 700
 Gly Pro Gly Ala Phe Asp Val Asn Thr Gly Pro Asn Trp Ala Thr Phe
 705 710 715 720
 Ile Lys Arg Phe Pro His Asn Pro Arg Asp Trp Asp Arg Leu Pro Tyr
 725 730 735
 Leu Asn Leu Pro Tyr Leu Pro Pro Asn Ala Gly Arg Gln Tyr His Leu
 740 745 750
 Ala Met Ala Ala Ser Glu Phe Lys Glu Thr Pro Glu Leu Glu Ser Ala
 755 760 765
 Val Arg Ala Met Glu Ala Ala Ala Asn Val Asp Pro Leu Phe Gln Ser
 770 775 780
 Ala Leu Ser Val Phe Met Trp Leu Glu Glu Asn Gly Ile Val Thr Asp
 785 790 795 800
 Met Ala Asn Phe Ala Leu Ser Asp Pro Asn Ala His Arg Met Arg Asn
 805 810 815
 Phe Leu Ala Asn Ala Pro Gln Ala Gly Ser Lys Ser Gln Arg Ala Lys
 820 825 830
 Tyr Gly Thr Ala Gly Tyr Gly Val Glu Ala Arg Gly Pro Thr Pro Glu
 835 840 845
 Glu Ala Gln Arg Glu Lys Asp Thr Arg Ile Ser Lys Lys Met Glu Thr
 850 855 860
 Met Gly Ile Tyr Phe Ala Thr Pro Glu Trp Val Ala Leu Asn Gly His
 865 870 875 880
 Arg Gly Pro Ser Pro Gly Gln Leu Lys Tyr Trp Gln Asn Thr Arg Glu
 885 890 895
 Ile Pro Asp Pro Asn Glu Asp Tyr Leu Asp Tyr Val His Ala Glu Lys
 900 905 910
 Ser Arg Leu Ala Ser Glu Glu Gln Ile Leu Arg Ala Ala Thr Ser Ile
 915 920 925
 Tyr Gly Ala Pro Gly Gln Ala Glu Pro Pro Gln Ala Phe Ile Asp Glu
 930 935 940
 Val Ala Lys Val Tyr Glu Ile Asn His Gly Arg Gly Pro Asn Gln Glu
 945 950 955 960
 Gln Met Lys Asp Leu Leu Leu Thr Ala Met Glu Met Lys His Arg Asn

Tyr Val Arg Leu Gly Asp Pro Ile Pro Ala Ile Gly Leu Asp Pro Lys
 180 185 190
 Met Val Ala Thr Cys Asp Ser Ser Asp Arg Pro Arg Val Tyr Thr Ile
 195 200 205
 Thr Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Ala Gly Gly
 210 215 220
 Val Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu
 225 230 235 240
 Ser Ile Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Ile
 245 250 255
 Leu Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile
 260 265 270
 Thr Arg Ala Val Ala Ala Asp Asn Gly Leu Thr Ala Gly Thr Asp Asn
 275 280 285
 Leu Met Pro Phe Asn Ile Val Ile Pro Thr Ser Glu Ile Thr Gln Pro
 290 295 300
 Ile Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln
 305 310 315 320
 Ala Gly Asp Gln Met Ser Trp Ser Ala Ser Gly Ser Leu Ala Val Thr
 325 330 335
 Ile His Gly Gly Asn Tyr Pro Gly Ala Leu Arg Pro Val Thr Leu Val
 340 345 350
 Ala Tyr Glu Arg Val Ala Thr Gly Ser Val Val Thr Val Ala Gly Val
 355 360 365
 Ser Asn Phe Glu Leu Ile Pro Asn Pro Glu Leu Ala Lys Asn Leu Val
 370 375 380
 Thr Glu Tyr Gly Arg Phe Asp Pro Gly Ala Met Asn Tyr Thr Lys Leu
 385 390 395 400
 Ile Leu Ser Glu Arg Asp Arg Leu Gly Ile Lys Thr Val Trp Pro Thr
 405 410 415
 Arg Glu Tyr Thr Asp Phe Arg Glu Tyr Phe Met Glu Val Ala Asp Leu
 420 425 430
 Asn Ser Pro Leu Lys Ile Ala Gly Ala Phe Gly Phe Lys Asp Ile Ile
 435 440 445
 Arg Ala Leu Arg Arg Ile Ala Val Pro Val Val Ser Thr Leu Phe Pro
 450 455 460

Pro Ala Ala Pro Leu Ala His Ala Ile Gly Glu Gly Val Asp Tyr Leu
 465 470 475 480
 Leu Gly Asp Glu Ala Gln Ala Ala Ser Gly Thr Ala Arg Ala Ala Ser
 485 490 495
 Gly Lys Ala Arg Ala Ala Ser Gly Arg Ile Arg Gln Leu Thr Leu Ala
 500 505 510
 Ala Asp Lys Gly Tyr Glu Val Val Ala Asn Leu Phe Gln Val Pro Gln
 515 520 525
 Asn Pro Val Val Asp Gly Ile Leu Ala Ser Pro Gly Ile Leu Arg Gly
 530 535 540
 Ala His Asn Leu Asp Cys Val Leu Arg Glu Gly Ala Thr Leu Phe Pro
 545 550 555 560
 Val Val Ile Thr Thr Val Glu Asp Ala Met Thr Pro Lys Ala Leu Asn
 565 570 575
 Ser Lys Met Phe Ala Val Ile Glu Gly Val Arg Glu Asp Leu Gln Pro
 580 585 590
 Pro Ser Gln Arg Gly Ser Phe Ile Arg Thr Leu Ser Gly His Arg Val
 595 600 605
 Tyr Gly Tyr Ala Pro Asp Gly Val Leu Pro Leu Glu Thr Gly Arg Asp
 610 615 620
 Tyr Thr Val Val Pro Ile Asp Asp Val Trp Asp Asp Ser Ile Met Leu
 625 630 635 640
 Ser Lys Asp Pro Ile Pro Pro Ile Val Gly Asn Ser Gly Asn Leu Ala
 645 650 655
 Ile Ala Tyr Met Asp Val Phe Arg Pro Lys Val Pro Ile His Val Ala
 660 665 670
 Met Thr Gly Ala Leu Asn Ala Tyr Gly Glu Ile Glu Asn Val Ser Phe
 675 680 685
 Arg Ser Thr Lys Leu Ala Thr Ala His Arg Leu Gly Leu Lys Leu Ala
 690 695 700
 Gly Pro Gly Ala Phe Asp Val Asn Thr Gly Ser Asn Trp Ala Thr Phe
 705 710 715 720
 Ile Lys Arg Phe Pro His Asn Pro Arg Asp Trp Asp Arg Leu Pro Tyr
 725 730 735
 Leu Asn Leu Pro Tyr Leu Pro Pro Asn Ala Gly Arg Gln Tyr Asp Leu
 740 745 750
 Ala Met Ala Ala Ser Glu Phe Lys Glu Thr Pro Glu Leu Glu Ser Ala

755					760					765						
Val	Arg	Ala	Met	Glu	Ala	Ala	Ala	Ala	Asn	Val	Asp	Pro	Leu	Phe	Gln	Ser
770							775					780				
Ala	Leu	Ser	Val	Phe	Met	Trp	Leu	Glu	Glu	Asn	Gly	Ile	Val	Thr	Asp	
785						790					795					800
Met	Ala	Asn	Phe	Ala	Leu	Ser	Asp	Pro	Asn	Ala	His	Arg	Met	Arg	Asn	
				805					810					815		
Phe	Leu	Ala	Asn	Ala	Pro	Gln	Ala	Gly	Ser	Lys	Ser	Gln	Arg	Ala	Lys	
			820					825						830		
Tyr	Gly	Thr	Ala	Gly	Tyr	Gly	Val	Glu	Ala	Arg	Gly	Pro	Thr	Pro	Glu	
		835					840					845				
Glu	Ala	Gln	Arg	Glu	Lys	Asp	Thr	Arg	Ile	Ser	Lys	Lys	Met	Glu	Thr	
		850				855					860					
Met	Gly	Ile	Tyr	Phe	Ala	Thr	Pro	Glu	Trp	Val	Ala	Leu	Asn	Gly	His	
865						870					875					880
Arg	Gly	Pro	Ser	Pro	Gly	Gln	Leu	Lys	Tyr	Trp	Gln	Asn	Thr	Arg	Glu	
				885					890					895		
Ile	Pro	Asp	Pro	Asn	Glu	Asp	Tyr	Leu	Asp	Tyr	Val	His	Ala	Glu	Lys	
			900					905					910			
Ser	Arg	Leu	Ala	Ser	Glu	Glu	Gln	Ile	Leu	Arg	Ala	Ala	Thr	Ser	Ile	
		915					920					925				
Tyr	Gly	Ala	Pro	Gly	Gln	Ala	Glu	Pro	Pro	Gln	Ala	Phe	Ile	Asp	Glu	
		930				935					940					
Val	Ala	Lys	Val	Tyr	Glu	Ile	Asn	His	Gly	Arg	Gly	Pro	Asn	Gln	Glu	
945						950					955					960
Gln	Met	Lys	Asp	Leu	Leu	Leu	Thr	Ala	Met	Glu	Met	Lys	His	Arg	Asn	
				965					970					975		
Pro	Arg	Arg	Ala	Pro	Pro	Lys	Pro	Lys	Pro	Lys	Pro	Asn	Ala	Pro	Thr	
			980					985					990			
Gln	Arg	Pro	Pro	Gly	Arg	Leu	Gly	Arg	Trp	Ile	Arg	Ala	Val	Ser	Asp	
		995					1000					1005				
Glu	Asp	Leu	Glu													
		1010														

<210> 80
 <211> 290
 <212> PRT
 <213> Infectious bursal disease virus

<220>

<221> DOMAIN

<222> (1)..(290)

<223> Sequence of IBDV polyprotein TY89-PP

<400> 80

Arg Phe Pro His Asn Pro Arg Asp Trp Asp Arg Leu Pro Tyr Leu Asn
1 5 10 15

Leu Pro Tyr Leu Pro Pro Thr Ala Gly Arg Gln Phe His Leu Ala Leu
20 25 30

Ala Ala Ser Glu Phe Lys Glu Thr Pro Glu Leu Glu Asp Ala Val Arg
35 40 45

Ala Met Asp Ala Ala Ala Asn Val Asp Pro Leu Phe Arg Ser Ala Leu
50 55 60

Gln Val Phe Met Trp Leu Glu Glu Asn Gly Ile Val Thr Asp Met Ala
65 70 75 80

Asn Phe Ala Leu Ser Asp Pro Asn Ala His Arg Met Lys Asn Phe Leu
85 90 95

Ala Asn Ala Pro Gln Ala Gly Ser Lys Ser Gln Arg Ala Lys Tyr Gly
100 105 110

Thr Ala Gly Tyr Gly Val Glu Ala Arg Gly Pro Thr Pro Glu Glu Ala
115 120 125

Gln Arg Glu Lys Asp Thr Arg Ile Ser Lys Lys Met Glu Thr Met Gly
130 135 140

Ile Tyr Phe Ala Thr Pro Glu Trp Val Ala Leu Asn Gly His Arg Gly
145 150 155 160

Pro Ser Pro Gly Gln Leu Lys Tyr Trp Gln Asn Thr Arg Glu Ile Pro
165 170 175

Glu Pro Asn Glu Asp Tyr Pro Asp Tyr Val His Ala Glu Lys Ser Arg
180 185 190

Leu Ala Ser Glu Glu Gln Val Leu Arg Ala Ala Thr Ser Ile Tyr Gly
195 200 205

Ala Pro Gly Gln Ala Glu Pro Pro Gln Ala Phe Ile Asp Glu Val Ala
210 215 220

Arg Val Tyr Glu Ile Asn His Gly Arg Gly Pro Asn Gln Glu Gln Met
225 230 235 240

Lys Asp Leu Leu Leu Thr Ala Met Glu Met Lys His Arg Asn Pro Arg
245 250 255

Arg Ala Pro Pro Lys Pro Lys Pro Lys Pro Asn Ala Pro Ser Gln Arg
260 265 270

Pro Pro Gly Arg Leu Gly Arg Trp Ile Arg Thr Val Ser Asp Glu Asp
275 280 285

Leu Glu
290

<210> 81
<211> 881
<212> PRT
<213> Infectious bursal disease virus

<220>
<221> DOMAIN
<222> (1)..(881)
<223> Consensus sequence of IBDV VP1

<220>
<221> MISC_FEATURE
<222> (4)
<223> The 'Xaa' at position 4 may be any amino acid

<220>
<221> MISC_FEATURE
<222> (13)
<223> The 'Xaa' at position 13 may be any amino acid

<220>
<221> MISC_FEATURE
<222> (61)
<223> The 'Xaa' at position 61 may be any amino acid

<220>
<221> MISC_FEATURE
<222> (145)..(147)
<223> The 'Xaa' at positions 145-147 may be any amino acid

<220>
<221> MISC_FEATURE
<222> (242)
<223> The 'Xaa' at position 242 may be any amino acid

<220>
<221> MISC_FEATURE
<222> (287)
<223> The 'Xaa' at position 287 may be any amino acid

<220>
<221> MISC_FEATURE
<222> (390)
<223> The 'Xaa' at position 390 may be any amino acid

<220>
 <221> MISC_FEATURE
 <222> (393)
 <223> The 'Xaa' at position 393 may be any amino acid

 <220>
 <221> MISC_FEATURE
 <222> (508)
 <223> The 'Xaa' at position 508 may be any amino acid

 <220>
 <221> MISC_FEATURE
 <222> (511)
 <223> The 'Xaa' at position 511 may be any amino acid

 <220>
 <221> MISC_FEATURE
 <222> (546)
 <223> The 'Xaa' at position 546 may be any amino acid

 <220>
 <221> MISC_FEATURE
 <222> (562)
 <223> The 'Xaa' at position 562 may be any amino acid

 <220>
 <221> MISC_FEATURE
 <222> (646)
 <223> The 'Xaa' at position 646 may be any amino acid

 <220>
 <221> MISC_FEATURE
 <222> (687)
 <223> The 'Xaa' at position 687 may be any amino acid

 <220>
 <221> MISC_FEATURE
 <222> (695)
 <223> The 'Xaa' at position 695 may be any amino acid

 <220>
 <221> MISC_FEATURE
 <222> (880) . . . (881)
 <223> The 'Xaa' at positions 880-881 may be any amino acid

<400> 81
 Met Ser Asp Xaa Phe Asn Ser Pro Gln Ala Arg Ser Xaa Ile Ser Ala
 1 5 10 15

 Ala Phe Gly Ile Lys Pro Thr Ala Gly Gln Asp Val Glu Glu Leu Leu
 20 25 30

 Ile Pro Lys Val Trp Val Pro Pro Glu Asp Pro Leu Ala Ser Pro Ser

35					40					45					
Arg	Leu	Ala	Lys	Phe	Leu	Arg	Glu	Asn	Gly	Tyr	Lys	Xaa	Leu	Gln	Pro
50						55					60				
Arg	Ser	Leu	Pro	Glu	Asn	Glu	Glu	Tyr	Glu	Thr	Asp	Gln	Ile	Leu	Pro
65					70					75					80
Asp	Leu	Ala	Trp	Met	Arg	Gln	Ile	Glu	Gly	Ala	Val	Leu	Lys	Pro	Thr
				85					90					95	
Leu	Ser	Leu	Pro	Ile	Gly	Asp	Gln	Glu	Tyr	Phe	Pro	Lys	Tyr	Tyr	Pro
			100					105					110		
Thr	His	Arg	Pro	Ser	Lys	Glu	Lys	Pro	Asn	Ala	Tyr	Pro	Pro	Asp	Ile
		115					120					125			
Ala	Leu	Leu	Lys	Gln	Met	Ile	Tyr	Leu	Phe	Leu	Gln	Val	Pro	Glu	Ala
	130					135					140				
Xaa	Xaa	Xaa	Leu	Lys	Asp	Glu	Val	Thr	Leu	Leu	Thr	Gln	Asn	Ile	Arg
145					150					155					160
Asp	Lys	Ala	Tyr	Gly	Ser	Gly	Thr	Tyr	Met	Gly	Gln	Ala	Thr	Arg	Leu
				165					170					175	
Val	Ala	Met	Lys	Glu	Val	Ala	Thr	Gly	Arg	Asn	Pro	Asn	Lys	Asp	Pro
		180						185					190		
Leu	Lys	Leu	Gly	Tyr	Thr	Phe	Glu	Ser	Ile	Ala	Gln	Leu	Leu	Asp	Ile
	195						200					205			
Thr	Leu	Pro	Val	Gly	Pro	Pro	Gly	Glu	Asp	Asp	Lys	Pro	Trp	Val	Pro
	210					215					220				
Leu	Thr	Arg	Val	Pro	Ser	Arg	Met	Leu	Val	Leu	Thr	Gly	Asp	Val	Asp
225					230					235					240
Gly	Xaa	Phe	Glu	Val	Glu	Asp	Tyr	Leu	Pro	Lys	Ile	Asn	Leu	Lys	Ser
			245						250					255	
Ser	Ser	Gly	Leu	Pro	Tyr	Val	Gly	Arg	Thr	Lys	Gly	Glu	Thr	Ile	Gly
			260					265					270		
Glu	Met	Ile	Ala	Ile	Ser	Asn	Gln	Phe	Leu	Arg	Glu	Leu	Ser	Xaa	Leu
	275						280					285			
Leu	Lys	Gln	Gly	Ala	Gly	Thr	Lys	Gly	Ser	Asn	Lys	Lys	Lys	Leu	Leu
	290					295					300				
Ser	Met	Leu	Ser	Asp	Tyr	Trp	Tyr	Leu	Ser	Cys	Gly	Leu	Leu	Phe	Pro
305					310					315					320
Lys	Ala	Glu	Arg	Tyr	Asp	Lys	Ser	Thr	Trp	Leu	Thr	Lys	Thr	Arg	Asn
				325					330					335	

Ile	Trp	Ser	Ala	Pro	Ser	Pro	Thr	His	Leu	Met	Ile	Ser	Met	Ile	Thr	340	345	350	
Trp	Pro	Val	Met	Ser	Asn	Ser	Pro	Asn	Asn	Val	Leu	Asn	Ile	Glu	Gly	355	360	365	
Cys	Pro	Ser	Leu	Tyr	Lys	Phe	Asn	Pro	Phe	Arg	Gly	Gly	Leu	Asn	Arg	370	375	380	
Ile	Val	Glu	Trp	Ile	Xaa	Ala	Pro	Xaa	Glu	Pro	Lys	Ala	Leu	Val	Tyr	385	390	395	400
Ala	Asp	Asn	Ile	Tyr	Ile	Val	His	Ser	Asn	Thr	Trp	Tyr	Ser	Ile	Asp	405	410	415	
Leu	Glu	Lys	Gly	Glu	Ala	Asn	Cys	Thr	Arg	Gln	His	Met	Gln	Ala	Ala	420	425	430	
Met	Tyr	Tyr	Ile	Leu	Thr	Arg	Gly	Trp	Ser	Asp	Asn	Gly	Asp	Pro	Met	435	440	445	
Phe	Asn	Gln	Thr	Trp	Ala	Thr	Phe	Ala	Met	Asn	Ile	Ala	Pro	Ala	Leu	450	455	460	
Val	Val	Asp	Ser	Ser	Cys	Leu	Ile	Met	Asn	Leu	Gln	Ile	Lys	Thr	Tyr	465	470	475	480
Gly	Gln	Gly	Ser	Gly	Asn	Ala	Ala	Thr	Phe	Ile	Asn	Asn	His	Leu	Leu	485	490	495	
Ser	Thr	Leu	Val	Leu	Asp	Gln	Trp	Asn	Leu	Met	Xaa	Gln	Pro	Xaa	Pro	500	505	510	
Asp	Ser	Glu	Glu	Phe	Lys	Ser	Ile	Glu	Asp	Lys	Leu	Gly	Ile	Asn	Phe	515	520	525	
Lys	Ile	Glu	Arg	Ser	Ile	Asp	Asp	Ile	Arg	Gly	Lys	Leu	Arg	Gln	Leu	530	535	540	
Val	Xaa	Leu	Ala	Gln	Pro	Gly	Tyr	Leu	Ser	Gly	Gly	Val	Glu	Pro	Glu	545	550	555	560
Gln	Xaa	Ser	Pro	Thr	Val	Glu	Leu	Asp	Leu	Leu	Gly	Trp	Ser	Ala	Thr	565	570	575	
Tyr	Ser	Lys	Asp	Leu	Gly	Ile	Tyr	Val	Pro	Val	Leu	Asp	Lys	Glu	Arg	580	585	590	
Leu	Phe	Cys	Ser	Ala	Ala	Tyr	Pro	Lys	Gly	Val	Glu	Asn	Lys	Ser	Leu	595	600	605	
Lys	Ser	Lys	Val	Gly	Ile	Glu	Gln	Ala	Tyr	Lys	Val	Val	Arg	Tyr	Glu	610	615	620	

Ala Leu Arg Leu Val Gly Gly Trp Asn Tyr Pro Leu Leu Asn Lys Ala
625 630 635 640

Cys Lys Asn Asn Ala Xaa Ala Ala Arg Arg His Leu Glu Ala Lys Gly
645 650 655

Phe Pro Leu Asp Glu Phe Leu Ala Glu Trp Ser Glu Leu Ser Glu Phe
660 665 670

Gly Glu Ala Phe Glu Gly Phe Asn Ile Lys Leu Thr Val Thr Xaa Glu
675 680 685

Ser Leu Ala Glu Leu Asn Xaa Pro Val Pro Pro Lys Pro Pro Asn Val
690 695 700

Asn Arg Pro Val Asn Thr Gly Gly Leu Lys Ala Val Ser Asn Ala Leu
705 710 715 720

Lys Thr Gly Arg Tyr Arg Asn Glu Ala Gly Leu Ser Gly Leu Val Leu
725 730 735

Leu Ala Thr Ala Arg Ser Arg Leu Gln Asp Ala Val Lys Ala Lys Ala
740 745 750

Glu Ala Glu Lys Leu His Lys Ser Lys Pro Asp Asp Pro Asp Ala Asp
755 760 765

Trp Phe Glu Arg Ser Glu Thr Leu Ser Asp Leu Leu Glu Lys Ala Asp
770 775 780

Ile Ala Ser Lys Val Ala His Ser Ala Leu Val Glu Thr Ser Asp Ala
785 790 795 800

Leu Glu Ala Val Gln Ser Thr Ser Val Tyr Thr Pro Lys Tyr Pro Glu
805 810 815

Val Lys Asn Pro Gln Thr Ala Ser Asn Pro Val Val Gly Leu His Leu
820 825 830

Pro Ala Lys Arg Ala Thr Gly Val Gln Ala Ala Leu Leu Gly Ala Gly
835 840 845

Thr Ser Arg Pro Met Gly Met Glu Ala Pro Thr Arg Ser Lys Asn Ala
850 855 860

Val Lys Met Ala Lys Arg Arg Gln Arg Gln Lys Glu Ser Arg Gln Xaa
865 870 875 880

Xaa

<210> 82

<211> 881

<212> PRT

<213> Infectious bursal disease virus

<220>

<221> DOMAIN

<222> (1)..(881)

<223> Sequence of IBDV CEF94-VP1

<400> 82

Met Ser Asp Ile Phe Asn Ser Pro Gln Ala Arg Ser Thr Ile Ser Ala
1 5 10 15

Ala Phe Gly Ile Lys Pro Thr Ala Gly Gln Asp Val Glu Glu Leu Leu
20 25 30

Ile Pro Lys Val Trp Val Pro Pro Glu Asp Pro Leu Ala Ser Pro Ser
35 40 45

Arg Leu Ala Lys Phe Leu Arg Glu Asn Gly Tyr Lys Val Leu Gln Pro
50 55 60

Arg Ser Leu Pro Glu Asn Glu Glu Tyr Glu Thr Asp Gln Ile Leu Pro
65 70 75 80

Asp Leu Ala Trp Met Arg Gln Ile Glu Gly Ala Val Leu Lys Pro Thr
85 90 95

Leu Ser Leu Pro Ile Gly Asp Gln Glu Tyr Phe Pro Lys Tyr Tyr Pro
100 105 110

Thr His Arg Pro Ser Lys Glu Lys Pro Asn Ala Tyr Pro Pro Asp Ile
115 120 125

Ala Leu Leu Lys Gln Met Ile Tyr Leu Phe Leu Gln Val Pro Glu Ala
130 135 140

Asn Glu Gly Leu Lys Asp Glu Val Thr Leu Leu Thr Gln Asn Ile Arg
145 150 155 160

Asp Lys Ala Tyr Gly Ser Gly Thr Tyr Met Gly Gln Ala Thr Arg Leu
165 170 175

Val Ala Met Lys Glu Val Ala Thr Gly Arg Asn Pro Asn Lys Asp Pro
180 185 190

Leu Lys Leu Gly Tyr Thr Phe Glu Ser Ile Ala Gln Leu Leu Asp Ile
195 200 205

Thr Leu Pro Val Gly Pro Pro Gly Glu Asp Asp Lys Pro Trp Val Pro
210 215 220

Leu Thr Arg Val Pro Ser Arg Met Leu Val Leu Thr Gly Asp Val Asp
225 230 235 240

Gly Asp Phe Glu Val Glu Asp Tyr Leu Pro Lys Ile Asn Leu Lys Ser

245										250					255				
Ser	Ser	Gly	Leu	Pro	Tyr	Val	Gly	Arg	Thr	Lys	Gly	Glu	Thr	Ile	Gly				
			260					265					270						
Glu	Met	Ile	Ala	Ile	Ser	Asn	Gln	Phe	Leu	Arg	Glu	Leu	Ser	Thr	Leu				
		275					280					285							
Leu	Lys	Gln	Gly	Ala	Gly	Thr	Lys	Gly	Ser	Asn	Lys	Lys	Lys	Leu	Leu				
	290					295					300								
Ser	Met	Leu	Ser	Asp	Tyr	Trp	Tyr	Leu	Ser	Cys	Gly	Leu	Leu	Phe	Pro				
305					310					315					320				
Lys	Ala	Glu	Arg	Tyr	Asp	Lys	Ser	Thr	Trp	Leu	Thr	Lys	Thr	Arg	Asn				
				325					330					335					
Ile	Trp	Ser	Ala	Pro	Ser	Pro	Thr	His	Leu	Met	Ile	Ser	Met	Ile	Thr				
			340					345					350						
Trp	Pro	Val	Met	Ser	Asn	Ser	Pro	Asn	Asn	Val	Leu	Asn	Ile	Glu	Gly				
		355					360					365							
Cys	Pro	Ser	Leu	Tyr	Lys	Phe	Asn	Pro	Phe	Arg	Gly	Gly	Leu	Asn	Arg				
	370					375					380								
Ile	Val	Glu	Trp	Ile	Leu	Ala	Pro	Glu	Glu	Pro	Lys	Ala	Leu	Val	Tyr				
385					390					395					400				
Ala	Asp	Asn	Ile	Tyr	Ile	Val	His	Ser	Asn	Thr	Trp	Tyr	Ser	Ile	Asp				
				405					410					415					
Leu	Glu	Lys	Gly	Glu	Ala	Asn	Cys	Thr	Arg	Gln	His	Met	Gln	Ala	Ala				
			420					425					430						
Met	Tyr	Tyr	Ile	Leu	Thr	Arg	Gly	Trp	Ser	Asp	Asn	Gly	Asp	Pro	Met				
		435					440					445							
Phe	Asn	Gln	Thr	Trp	Ala	Thr	Phe	Ala	Met	Asn	Ile	Ala	Pro	Ala	Leu				
	450					455					460								
Val	Val	Asp	Ser	Ser	Cys	Leu	Ile	Met	Asn	Leu	Gln	Ile	Lys	Thr	Tyr				
465					470					475					480				
Gly	Gln	Gly	Ser	Gly	Asn	Ala	Ala	Thr	Phe	Ile	Asn	Asn	His	Leu	Leu				
				485					490					495					
Ser	Thr	Leu	Val	Leu	Asp	Gln	Trp	Asn	Leu	Met	Arg	Gln	Pro	Arg	Pro				
			500					505					510						
Asp	Ser	Glu	Glu	Phe	Lys	Ser	Ile	Glu	Asp	Lys	Leu	Gly	Ile	Asn	Phe				
		515					520					525							
Lys	Ile	Glu	Arg	Ser	Ile	Asp	Asp	Ile	Arg	Gly	Lys	Leu	Arg	Gln	Leu				
	530					535					540								

Val Leu Leu Ala Gln Pro Gly Tyr Leu Ser Gly Gly Val Glu Pro Glu
545 550 555 560

Gln Ser Ser Pro Thr Val Glu Leu Asp Leu Leu Gly Trp Ser Ala Thr
565 570 575

Tyr Ser Lys Asp Leu Gly Ile Tyr Val Pro Val Leu Asp Lys Glu Arg
580 585 590

Leu Phe Cys Ser Ala Ala Tyr Pro Lys Gly Val Glu Asn Lys Ser Leu
595 600 605

Lys Ser Lys Val Gly Ile Glu Gln Ala Tyr Lys Val Val Arg Tyr Glu
610 615 620

Ala Leu Arg Leu Val Gly Gly Trp Asn Tyr Pro Leu Leu Asn Lys Ala
625 630 635 640

Cys Lys Asn Asn Ala Gly Ala Ala Arg Arg His Leu Glu Ala Lys Gly
645 650 655

Phe Pro Leu Asp Glu Phe Leu Ala Glu Trp Ser Glu Leu Ser Glu Phe
660 665 670

Gly Glu Ala Phe Glu Gly Phe Asn Ile Lys Leu Thr Val Thr Ser Glu
675 680 685

Ser Leu Ala Glu Leu Asn Lys Pro Val Pro Pro Lys Pro Pro Asn Val
690 695 700

Asn Arg Pro Val Asn Thr Gly Gly Leu Lys Ala Val Ser Asn Ala Leu
705 710 715 720

Lys Thr Gly Arg Tyr Arg Asn Glu Ala Gly Leu Ser Gly Leu Val Leu
725 730 735

Leu Ala Thr Ala Arg Ser Arg Leu Gln Asp Ala Val Lys Ala Lys Ala
740 745 750

Glu Ala Glu Lys Leu His Lys Ser Lys Pro Asp Asp Pro Asp Ala Asp
755 760 765

Trp Phe Glu Arg Ser Glu Thr Leu Ser Asp Leu Leu Glu Lys Ala Asp
770 775 780

Ile Ala Ser Lys Val Ala His Ser Ala Leu Val Glu Thr Ser Asp Ala
785 790 795 800

Leu Glu Ala Val Gln Ser Thr Ser Val Tyr Thr Pro Lys Tyr Pro Glu
805 810 815

Val Lys Asn Pro Gln Thr Ala Ser Asn Pro Val Val Gly Leu His Leu
820 825 830

Pro Ala Lys Arg Ala Thr Gly Val Gln Ala Ala Leu Leu Gly Ala Gly
835 840 845

Thr Ser Arg Pro Met Gly Met Glu Ala Pro Thr Arg Ser Lys Asn Ala
850 855 860

Val Lys Met Ala Lys Arg Arg Gln Arg Gln Lys Glu Ser Arg Gln Gln
865 870 875 880

Pro

<210> 83
<211> 879
<212> PRT
<213> Infectious bursal disease virus

<220>
<221> DOMAIN
<222> (1)..(879)
<223> Sequence of IBDV D6948-VP1

<400> 83
Met Ser Asp Val Phe Asn Ser Pro Gln Ala Arg Ser Lys Ile Ser Ala
1 5 10 15

Ala Phe Gly Ile Lys Pro Thr Ala Gly Gln Asp Val Glu Glu Leu Leu
20 25 30

Ile Pro Lys Val Trp Val Pro Pro Glu Asp Pro Leu Ala Ser Pro Ser
35 40 45

Arg Leu Ala Lys Phe Leu Arg Glu Asn Gly Tyr Lys Ile Leu Gln Pro
50 55 60

Arg Ser Leu Pro Glu Asn Glu Glu Tyr Glu Thr Asp Gln Ile Leu Pro
65 70 75 80

Asp Leu Ala Trp Met Arg Gln Ile Glu Gly Ala Val Leu Lys Pro Thr
85 90 95

Leu Ser Leu Pro Ile Gly Asp Gln Glu Tyr Phe Pro Lys Tyr Tyr Pro
100 105 110

Thr His Arg Pro Ser Lys Glu Lys Pro Asn Ala Tyr Pro Pro Asp Ile
115 120 125

Ala Leu Leu Lys Gln Met Ile Tyr Leu Phe Leu Gln Val Pro Glu Ala
130 135 140

Thr Asp Asn Leu Lys Asp Glu Val Thr Leu Leu Thr Gln Asn Ile Arg
145 150 155 160

Asp Lys Ala Tyr Gly Ser Gly Thr Tyr Met Gly Gln Ala Thr Arg Leu

165										170					175															
Val	Ala	Met	Lys	Glu	Val	Ala	Thr	Gly	Arg	Asn	Pro	Asn	Lys	Asp	Pro															
			180					185					190																	
Leu	Lys	Leu	Gly	Tyr	Thr	Phe	Glu	Ser	Ile	Ala	Gln	Leu	Leu	Asp	Ile															
		195					200					205																		
Thr	Leu	Pro	Val	Gly	Pro	Pro	Gly	Glu	Asp	Asp	Lys	Pro	Trp	Val	Pro															
	210					215					220																			
Leu	Thr	Arg	Val	Pro	Ser	Arg	Met	Leu	Val	Leu	Thr	Gly	Asp	Val	Asp															
225					230					235					240															
Gly	Glu	Phe	Glu	Val	Glu	Asp	Tyr	Leu	Pro	Lys	Ile	Asn	Leu	Lys	Ser															
				245					250					255																
Ser	Ser	Gly	Leu	Pro	Tyr	Val	Gly	Arg	Thr	Lys	Gly	Glu	Thr	Ile	Gly															
			260					265					270																	
Glu	Met	Ile	Ala	Ile	Ser	Asn	Gln	Phe	Leu	Arg	Glu	Leu	Ser	Ala	Leu															
		275					280					285																		
Leu	Lys	Gln	Gly	Ala	Gly	Thr	Lys	Gly	Ser	Asn	Lys	Lys	Lys	Leu	Leu															
	290					295					300																			
Ser	Met	Leu	Ser	Asp	Tyr	Trp	Tyr	Leu	Ser	Cys	Gly	Leu	Leu	Phe	Pro															
305					310					315					320															
Lys	Ala	Glu	Arg	Tyr	Asp	Lys	Ser	Thr	Trp	Leu	Thr	Lys	Thr	Arg	Asn															
				325					330					335																
Ile	Trp	Ser	Ala	Pro	Ser	Pro	Thr	His	Leu	Met	Ile	Ser	Met	Ile	Thr															
			340					345					350																	
Trp	Pro	Val	Met	Ser	Asn	Ser	Pro	Asn	Asn	Val	Leu	Asn	Ile	Glu	Gly															
		355					360					365																		
Cys	Pro	Ser	Leu	Tyr	Lys	Phe	Asn	Pro	Phe	Arg	Gly	Gly	Leu	Asn	Arg															
		370				375					380																			
Ile	Val	Glu	Trp	Ile	Met	Ala	Pro	Asp	Glu	Pro	Lys	Ala	Leu	Val	Tyr															
385					390				395						400															
Ala	Asp	Asn	Ile	Tyr	Ile	Val	His	Ser	Asn	Thr	Trp	Tyr	Ser	Ile	Asp															
				405					410					415																
Leu	Glu	Lys	Gly	Glu	Ala	Asn	Cys	Thr	Arg	Gln	His	Met	Gln	Ala	Ala															
			420					425					430																	
Met	Tyr	Tyr	Ile	Leu	Thr	Arg	Gly	Trp	Ser	Asp	Asn	Gly	Asp	Pro	Met															
		435					440					445																		
Phe	Asn	Gln	Thr	Trp	Ala	Thr	Phe	Ala	Met	Asn	Ile	Ala	Pro	Ala	Leu															
		450				455					460																			

Val	Val	Asp	Ser	Ser	Cys	Leu	Ile	Met	Asn	Leu	Gln	Ile	Lys	Thr	Tyr	
465					470					475					480	
Gly	Gln	Gly	Ser	Gly	Asn	Ala	Ala	Thr	Phe	Ile	Asn	Asn	His	Leu	Leu	
				485					490					495		
Ser	Thr	Leu	Val	Leu	Asp	Gln	Trp	Asn	Leu	Met	Lys	Gln	Pro	Ser	Pro	
			500					505					510			
Asp	Ser	Glu	Glu	Phe	Lys	Ser	Ile	Glu	Asp	Lys	Leu	Gly	Ile	Asn	Phe	
		515					520					525				
Lys	Ile	Glu	Arg	Ser	Ile	Asp	Asp	Ile	Arg	Gly	Lys	Leu	Arg	Gln	Leu	
	530					535						540				
Val	Pro	Leu	Ala	Gln	Pro	Gly	Tyr	Leu	Ser	Gly	Gly	Val	Glu	Pro	Glu	
545					550					555					560	
Gln	Pro	Ser	Pro	Thr	Val	Glu	Leu	Asp	Leu	Leu	Gly	Trp	Ser	Ala	Thr	
				565					570					575		
Tyr	Ser	Lys	Asp	Leu	Gly	Ile	Tyr	Val	Pro	Val	Leu	Asp	Lys	Glu	Arg	
			580					585					590			
Leu	Phe	Cys	Ser	Ala	Ala	Tyr	Pro	Lys	Gly	Val	Glu	Asn	Lys	Ser	Leu	
		595					600					605				
Lys	Ser	Lys	Val	Gly	Ile	Glu	Gln	Ala	Tyr	Lys	Val	Val	Arg	Tyr	Glu	
	610					615					620					
Ala	Leu	Arg	Leu	Val	Gly	Gly	Trp	Asn	Tyr	Pro	Leu	Leu	Asn	Lys	Ala	
625					630					635					640	
Cys	Lys	Asn	Asn	Ala	Ser	Ala	Ala	Arg	Arg	His	Leu	Glu	Ala	Lys	Gly	
				645					650					655		
Phe	Pro	Leu	Asp	Glu	Phe	Leu	Ala	Glu	Trp	Ser	Glu	Leu	Ser	Glu	Phe	
			660					665					670			
Gly	Glu	Ala	Phe	Glu	Gly	Phe	Asn	Ile	Lys	Leu	Thr	Val	Thr	Pro	Glu	
		675					680					685				
Ser	Leu	Ala	Glu	Leu	Asn	Arg	Pro	Val	Pro	Pro	Lys	Pro	Pro	Asn	Val	
	690					695					700					
Asn	Arg	Pro	Val	Asn	Thr	Gly	Gly	Leu	Lys	Ala	Val	Ser	Asn	Ala	Leu	
705					710					715					720	
Lys	Thr	Gly	Arg	Tyr	Arg	Asn	Glu	Ala	Gly	Leu	Ser	Gly	Leu	Val	Leu	
				725					730					735		
Leu	Ala	Thr	Ala	Arg	Ser	Arg	Leu	Gln	Asp	Ala	Val	Lys	Ala	Lys	Ala	
			740					745					750			

Glu Ala Glu Lys Leu His Lys Ser Lys Pro Asp Asp Pro Asp Ala Asp
 755 760 765
 Trp Phe Glu Arg Ser Glu Thr Leu Ser Asp Leu Leu Glu Lys Ala Asp
 770 775 780
 Ile Ala Ser Lys Val Ala His Ser Ala Leu Val Glu Thr Ser Asp Ala
 785 790 795 800
 Leu Glu Ala Val Gln Ser Thr Ser Val Tyr Thr Pro Lys Tyr Pro Glu
 805 810 815
 Val Lys Asn Pro Gln Thr Ala Ser Asn Pro Val Val Gly Leu His Leu
 820 825 830
 Pro Ala Lys Arg Ala Thr Gly Val Gln Ala Ala Leu Leu Gly Ala Gly
 835 840 845
 Thr Ser Arg Pro Met Gly Met Glu Ala Pro Thr Arg Ser Lys Asn Ala
 850 855 860
 Val Lys Met Ala Lys Arg Arg Gln Arg Gln Lys Glu Ser Arg Gln
 865 870 875

<210> 84
 <211> 145
 <212> PRT
 <213> Infectious bursal disease virus

<220>
 <221> DOMAIN
 <222> (1)..(145)
 <223> Consensus sequence of IBDV VP5

<220>
 <221> MISC_FEATURE
 <222> (14)
 <223> The 'Xaa' at position 14 may be any amino acid

<220>
 <221> MISC_FEATURE
 <222> (45)
 <223> The 'Xaa' at position 45 may be any amino acid

<220>
 <221> MISC_FEATURE
 <222> (74)
 <223> The 'Xaa' at position 74 may be any amino acid

<220>
 <221> MISC_FEATURE
 <222> (125)
 <223> The 'Xaa' at position 125 may be any amino acid

<220>
 <221> MISC_FEATURE
 <222> (133)
 <223> The 'Xaa' at position 133 may be any amino acid

<400> 84
 Met Val Ser Arg Asp Gln Thr Asn Asp Arg Ser Asp Asp Xaa Pro Ala
 1 5 10 15
 Arg Ser Asn Pro Thr Asp Cys Ser Val His Thr Glu Pro Ser Asp Ala
 20 25 30
 Asn Asn Arg Thr Gly Val His Ser Gly Arg His Pro Xaa Glu Ala His
 35 40 45
 Ser Gln Val Arg Asp Leu Asp Leu Gln Phe Asp Cys Gly Gly His Arg
 50 55 60
 Val Arg Ala Asn Cys Leu Phe Pro Trp Xaa Pro Trp Leu Asn Cys Gly
 65 70 75 80
 Cys Ser Leu His Thr Ala Glu Gln Trp Glu Leu Gln Val Arg Ser Asp
 85 90 95
 Ala Pro Asp Cys Pro Glu Pro Thr Gly Gln Leu Gln Leu Leu Gln Ala
 100 105 110
 Ser Glu Ser Glu Ser His Ser Glu Val Lys His Thr Xaa Trp Trp Arg
 115 120 125
 Leu Cys Thr Lys Xaa His His Lys Arg Arg Asp Leu Pro Arg Lys Pro
 130 135 140
 Glu
 145

<210> 85
 <211> 145
 <212> PRT
 <213> Infectious bursal disease virus

<220>
 <221> DOMAIN
 <222> (1)..(145)
 <223> Sequence of IBV D6948-VP5

<400> 85
 Met Val Ser Arg Asp Gln Thr Asn Asp Arg Ser Asp Asp Glu Pro Ala
 1 5 10 15
 Arg Ser Asn Pro Thr Asp Cys Ser Val His Thr Glu Pro Ser Asp Ala

	20		25		30										
Asn	Asn	Arg	Thr	Gly	Val	His	Ser	Gly	Arg	His	Pro	Arg	Glu	Ala	His
	35						40					45			
Ser	Gln	Val	Arg	Asp	Leu	Asp	Leu	Gln	Phe	Asp	Cys	Gly	Gly	His	Arg
	50					55					60				
Val	Arg	Ala	Asn	Cys	Leu	Phe	Pro	Trp	Phe	Pro	Trp	Leu	Asn	Cys	Gly
	65				70					75					80
Cys	Ser	Leu	His	Thr	Ala	Glu	Gln	Trp	Glu	Leu	Gln	Val	Arg	Ser	Asp
			85						90					95	
Ala	Pro	Asp	Cys	Pro	Glu	Pro	Thr	Gly	Gln	Leu	Gln	Leu	Leu	Gln	Ala
			100					105						110	
Ser	Glu	Ser	Glu	Ser	His	Ser	Glu	Val	Lys	His	Thr	Pro	Trp	Trp	Arg
	115						120					125			
Leu	Cys	Thr	Lys	Trp	His	His	Lys	Arg	Arg	Asp	Leu	Pro	Arg	Lys	Pro
	130					135					140				
Glu															
145															

<210> 86
 <211> 145
 <212> PRT
 <213> Infectious bursal disease virus

<220>
 <221> DOMAIN
 <222> (1)..(145)
 <223> Sequence of IBV CEF94-VP5

<400> 86															
Met	Val	Ser	Arg	Asp	Gln	Thr	Asn	Asp	Arg	Ser	Asp	Asp	Lys	Pro	Ala
1				5					10					15	
Arg	Ser	Asn	Pro	Thr	Asp	Cys	Ser	Val	His	Thr	Glu	Pro	Ser	Asp	Ala
			20					25					30		
Asn	Asn	Arg	Thr	Gly	Val	His	Ser	Gly	Arg	His	Pro	Gly	Glu	Ala	His
		35					40					45			
Ser	Gln	Val	Arg	Asp	Leu	Asp	Leu	Gln	Phe	Asp	Cys	Gly	Gly	His	Arg
	50					55					60				
Val	Arg	Ala	Asn	Cys	Leu	Phe	Pro	Trp	Ile	Pro	Trp	Leu	Asn	Cys	Gly
	65				70					75					80
Cys	Ser	Leu	His	Thr	Ala	Glu	Gln	Trp	Glu	Leu	Gln	Val	Arg	Ser	Asp
				85					90					95	

Ala Pro Asp Cys Pro Glu Pro Thr Gly Gln Leu Gln Leu Leu Gln Ala
100 105 110

Ser Glu Ser Glu Ser His Ser Glu Val Lys His Thr Ser Trp Trp Arg
115 120 125

Leu Cys Thr Lys Arg His His Lys Arg Arg Asp Leu Pro Arg Lys Pro
130 135 140

Glu
145

<210> 87
<211> 149
<212> PRT
<213> Infectious bursal disease virus

<220>
<221> DOMAIN
<222> (1)..(149)
<223> Sequence of IBV D6948-VP5

<400> 87
Met Leu Ser Leu Met Val Ser Arg Asp Gln Thr Asn Asp Arg Ser Asp
1 5 10 15

Asp Glu Pro Ala Arg Ser Asn Pro Thr Asp Cys Ser Val His Thr Glu
20 25 30

Pro Ser Asp Ala Asn Asn Arg Thr Gly Val His Ser Gly Arg His Pro
35 40 45

Arg Glu Ala His Ser Gln Val Arg Asp Leu Asp Leu Gln Phe Asp Cys
50 55 60

Gly Gly His Arg Val Arg Ala Asn Cys Leu Phe Pro Trp Phe Pro Trp
65 70 75 80

Leu Asn Cys Gly Cys Ser Leu His Thr Ala Glu Gln Trp Glu Leu Gln
85 90 95

Val Arg Ser Asp Ala Pro Asp Cys Pro Glu Pro Thr Gly Gln Leu Gln
100 105 110

Leu Leu Gln Ala Ser Glu Ser Glu Ser His Ser Glu Val Lys His Thr
115 120 125

Pro Trp Trp Arg Leu Cys Thr Lys Trp His His Lys Arg Arg Asp Leu
130 135 140

Pro Arg Lys Pro Glu
145



11

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of:

Boot et al.

Serial No.: 10/046,671

Filed: January 14, 2002

For: MOSAIC INFECTIOUS BURSAL
DISEASE VIRUS VACCINES

Examiner: To be assigned

Group Art Unit: 1642

Attorney Docket No.: 2183-5238US

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Express Mail Mailing Label Number: EV175437543US

Date of Deposit with USPS: October 10, 2002

Person making Deposit: Orlena Howell

SEQUENCE STATEMENT

U.S. Patent and Trademark Office
Arlington, VA 22202

Sir:

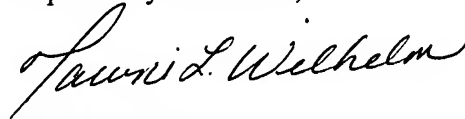
I, Tawni L. Wilhelm, an attorney registered to practice before the United States Patent & Trademark Office and attorney of record for this application, state that:

1. The enclosed paper copy of the substitute SEQUENCE LISTING, as well as the enclosed copy of the substitute SEQUENCE LISTING in computer readable form (CRF), have been prepared to comply with the requirements of 37 C.F.R. §§ 1.822 and/or 1.823.

2. The enclosed paper copy of the substitute SEQUENCE LISTING in computer readable form (CRF) is believed to be the same as the paper copy of the substitute SEQUENCE LISTING.

3. The SEQUENCE LISTING submitted herewith is believed to contain no "new matter" with regard to the referenced patent application. Modifications were made in response to the Notice to Comply. Such modifications include a change in the line indicator of SEQ ID NO: 53 to reflect that the sequence contains 8 nucleotides and not 7, a more particular delineation in the "Features" portion of SEQ ID NOS: 77, 81 and 84 to indicate which amino acid positions contain the "Xaa" indicator and what it means, and a deletion of the spaces following the last line of SEQ ID NO: 87.

Respectfully submitted,



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ACT/TLW/